



#6

## SEQUENCE LISTING

&lt;110&gt; Terek, Richard M.

&lt;120&gt; CHONDROSARCOMA ASSOCIATED GENES

&lt;130&gt; 21486-021DIV

&lt;140&gt; US 09/819,144

&lt;141&gt; 2001-03-27

&lt;160&gt; 8

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 164

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(156)

&lt;400&gt; 1

atg gct gcg ggt ccc agg cca gga gct ccc tgc agg gcg ggg gct ccc  
48Met Ala Ala Gly Pro Arg Pro Gly Ala Pro Cys Arg Ala Gly Ala Pro  
1 5 10 15acg atc gta ttg acc tct gga aga aga cag aca ctt tcc cac ggg agc  
96Thr Ile Val Leu Thr Ser Gly Arg Arg Gln Thr Leu Ser His Gly Ser  
20 25 30tcc tct cca gcc aga gct aca ctt ggc aaa cct ttg gtc cta aat gat  
144Ser Ser Pro Ala Arg Ala Thr Leu Gly Lys Pro Leu Val Leu Asn Asp  
35 40 45tat tca ctg aat tgaagaaa  
164Tyr Ser Leu Asn  
50

&lt;210&gt; 2

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met Ala Ala Gly Pro Arg Pro Gly Ala Pro Cys Arg Ala Gly Ala Pro  
1 5 10 15Thr Ile Val Leu Thr Ser Gly Arg Arg Gln Thr Leu Ser His Gly Ser  
20 25 30

Ser Ser Pro Ala Arg Ala Thr Leu Gly Lys Pro Leu Val Leu Asn Asp  
35 40 45  
Tyr Ser Leu Asn  
50

<210> 3  
<211> 884  
<212> DNA  
<213> Homo sapiens

<400> 3  
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60  
aggtggagct gcaccccttg tagagaatgg ctgcgggtcc caggccagga gtcctctgca  
120  
gggcgggggc tcccacgatc gtattgacct ctggaagaag acagacactt tcccacggga  
180  
gctcctctcc agccagagct acacttggca aacctttggt cctaaatgat tattcactga  
240  
attgaagaaa tacggtttac atatcttcca agtatatatg tagggttgat ttgggaagca  
300  
gaacacagca gcccaaattt gcttgtaatg tctgcgacta cagcctgctg gcctgccttc  
360  
actgtcttgg gggaagctcg gggagaccag gtggactgga gtagactgtg cagagacact  
420  
ggtctggtga agatgtccag gaaaccacga gcctccagcc cattttccaa caaccacca  
480  
tcaacaccaa agaggttccc aagacaaccc agaagggaaa agggaccctg caaggaagtt  
540  
ccaggaacaa aaggctctcc ctaaaagacc accgcttcaa aaaaacctga ggaatggagt  
600  
gggccaacac tatccagcca ctctgaccag ccgaacgagg aactcaatca aaatgcgcca  
660  
tagcaggacc acaagggcaa ggagaccacc gccttctcca gtgcttcctt gggcagccag  
720  
taattcccag gcaaggccag agacttcaag tctatctgaa aagtctccag aagtctaacc  
780  
ccagataaat agccaacagg gtgtagagta cgtttttacac ccaaagggtg atgccccatg  
840  
gtgatggaaa taaaatgaac atgttgtaaa atgaaaaaaaa aaaa  
884

<210> 4  
<211> 14  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Artificial sequence

<220>  
<221> misc\_feature  
<222> (1)...(14)  
<223> n = A,T,C or G

<400> 4

tttttttttt ttvn  
14

<210> 5  
<211> 1946  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(1946)  
<223> n = A,T,C or G

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60  
tggtgctgtt ggagactcga ttgttggtga cagcgaaaga acgataacaa aatgccggag  
120  
cgagatagtg agccgttctc caaccctttg gccccgatg gccacgatgt ggatgacct  
180  
cactccttcc accaatcaaa actcaccaat gaagacttca ggaaantnnt catgaccccc  
240  
agggntgcac ntacntntgc accacnttnt aantnnnntc accatgagat gccaagggag  
300  
tacaatgagg atgaagaccc agctgcacga aggaggaaaa agaaaagtta ttatgccaag  
360  
ctacgccaac aagaaattga gagagagaga gagctagcag agaagtaccg ggatcgtgcc  
420  
aaggaacgga gagatggagt gaacaaagat tatgaagaaa ccgagcttat cagcaccaca  
480  
gctaactata gggctgttgg cccactgct gaggcggaca aatcagctrc agnnragaga  
540  
agacanwnda hcnaggagtc caaattcttg ggtggtgaca tggaacacac ccatttggtg  
600  
aaaggcttgg attttgntnt gcttchnaan gtncgagctg agattgncms cmnanaraaa  
660  
nargaarang nnctgatggn aaanccccmg aaagaaacca agaaagatga ggatcctgaa  
720  
aataaaattg aatttaaaac acgtctgggc cgcaatgttt accgaatgct ttttaagagc  
780  
aaagcatatg agcggaatga gttgttcctg ccgggcccga tggcctatgt ggtagacctg  
840  
gatgatgagt atgctgacac agatatcccc accactctta tcccgcagca aggctgattg  
900  
ccccaccatg gaggcccaga ccacactgac cacaaatgac attgtcatta gcaagctgac  
960  
ccagatcctt tcatacctga ggcagggaac ccgtaacaag aagcttaaga agaaggataa  
1020  
agggaagccg gaagagaaga aacctcctga ggctgacatg aatatttttg aagacattgg  
1080  
ggattacgta ccctccacaa ccaagacacc tcgggacaag gagcgggaga gatatcggga  
1140  
acgggagcgt gatcgggaaa gagacagaga ccgtgaccga gagcgagagc gagaacgaga  
1200  
tcgggaacga gagcgagagc gggaccgaga gagagaagag gaaaagaaga gacacagcta  
1260

ctttgagaag ccaaaagtag atgatgagcc catggacgtt gacaaaggac ctgggtctac  
 1320  
 caaggagttg atcaagtcca tcaatgaaaa gtttgctggg tctgctggct gggaaggcac  
 1380  
 agaatcgctg aagaagccag aagacaaaaa gcagctggga gatttctttg gcatgtccaa  
 1440  
 cagttatgca gagtgctacc cagccacgat ggatgacatg gctgtggata gtgatgagga  
 1500  
 ggtggattat agcaaatgg accagggtaa caagaagggg cccttaggcc gttgggactt  
 1560  
 tgatacccag gaagaataca gcgagtatat gaacaacaaa gaagctttgc ccaaggctgc  
 1620  
 attccagtat ggtatcaaaa tgtctgaagg gcggaaaacc aggcgcttca aggaaaccaa  
 1680  
 tgacaaagca gagcttgatc gccagtggaa gaagattagt gcaatcattg angaagagga  
 1740  
 agaagatgga agctgatggg gttgaagtca aaagacccaa atactaatca ctagttacaa  
 1800  
 ccagagatgc tccacaagga tatgctcccc actgttttct ttctacaatt tccaaagggt  
 1860  
 gcaagatggt tttttgtgat gaatataaaa ttttattgtg taattacttg gttccattaa  
 1920  
 aattgggttaa cttgctaaaa aaaaaa  
 1946

<210> 6  
 <211> 915  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)...(912)

<220>  
 <221> misc\_feature  
 <222> (1)...(915)  
 <223> n = A,T,C or G

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 48  
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 1 5 10 15  
 aag gct gat tgc ccc acc atg gag gcc cag acc aca ctg acc aca aat  
 96  
 Lys Ala Asp Cys Pro Thr Met Glu Ala Gln Thr Thr Leu Thr Thr Asn  
 20 25 30  
 gac att gtc att agc aag ctg acc cag atc ctt tca tac ctg agg cag  
 144  
 Asp Ile Val Ile Ser Lys Leu Thr Gln Ile Leu Ser Tyr Leu Arg Gln  
 35 40 45  
 gga acc cgt aac aag aag ctt aag aag aag gat aaa ggg aag ccg gaa  
 192

Gly	Thr	Arg	Asn	Lys	Lys	Leu	Lys	Lys	Lys	Asp	Lys	Gly	Lys	Pro	Glu
50						55					60				
gag aag aaa cct cct gag gct gac atg aat att ttt gaa gac att ggg															
240															
Glu	Lys	Lys	Pro	Pro	Glu	Ala	Asp	Met	Asn	Ile	Phe	Glu	Asp	Ile	Gly
65					70				75						80
gat tac gta ccc tcc aca acc aag aca cct cgg gac aag gag cgg gag															
288															
Asp	Tyr	Val	Pro	Ser	Thr	Thr	Lys	Thr	Pro	Arg	Asp	Lys	Glu	Arg	Glu
				85					90					95	
aga tat cgg gaa cgg gag cgt gat cgg gaa aga gac aga gac cgt gac															
336															
Arg	Tyr	Arg	Glu	Arg	Glu	Arg	Asp	Arg	Glu	Arg	Asp	Arg	Asp	Arg	Asp
			100				105					110			
cga gag cga gag cga gaa cga gat cgg gaa cga gag cga gag cgg gac															
384															
Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp
		115					120					125			
cga gag aga gaa gag gaa aag aag aga cac agc tac ttt gag aag cca															
432															
Arg	Glu	Arg	Glu	Glu	Glu	Lys	Lys	Arg	His	Ser	Tyr	Phe	Glu	Lys	Pro
	130					135					140				
aaa gta gat gat gag ccc atg gac gtt gac aaa gga cct ggg tct acc															
480															
Lys	Val	Asp	Asp	Glu	Pro	Met	Asp	Val	Asp	Lys	Gly	Pro	Gly	Ser	Thr
145					150					155					160
aag gag ttg atc aag tcc atc aat gaa aag ttt gct ggg tct gct ggc															
528															
Lys	Glu	Leu	Ile	Lys	Ser	Ile	Asn	Glu	Lys	Phe	Ala	Gly	Ser	Ala	Gly
			165						170					175	
tgg gaa ggc aca gaa tcg ctg aag aag cca gaa gac aaa aag cag ctg															
576															
Trp	Glu	Gly	Thr	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Asp	Lys	Lys	Gln	Leu
			180					185					190		
gga gat ttc ttt ggc atg tcc aac agt tat gca gag tgc tac cca gcc															
624															
Gly	Asp	Phe	Phe	Gly	Met	Ser	Asn	Ser	Tyr	Ala	Glu	Cys	Tyr	Pro	Ala
		195					200					205			
acg atg gat gac atg gct gtg gat agt gat gag gag gtg gat tat agc															
672															
Thr	Met	Asp	Asp	Met	Ala	Val	Asp	Ser	Asp	Glu	Glu	Val	Asp	Tyr	Ser
	210					215					220				
aaa atg gac cag ggt aac aag aag ggg ccc tta ggc cgt tgg gac ttt															
720															
Lys	Met	Asp	Gln	Gly	Asn	Lys	Lys	Gly	Pro	Leu	Gly	Arg	Trp	Asp	Phe
225					230					235					240

gat acc cag gaa gaa tac agc gag tat atg aac aac aaa gaa gct ttg  
768

Asp Thr Gln Glu Glu Tyr Ser Glu Tyr Met Asn Asn Lys Glu Ala Leu  
245 250 255

ccc aag gct gca ttc cag tat ggt atc aaa atg tct gaa ggg cgg aaa  
816

Pro Lys Ala Ala Phe Gln Tyr Gly Ile Lys Met Ser Glu Gly Arg Lys  
260 265 270

acc agg cgc ttc aag gaa acc aat gac aaa gca gag ctt gat cgc cag  
864

Thr Arg Arg Phe Lys Glu Thr Asn Asp Lys Ala Glu Leu Asp Arg Gln  
275 280 285

tgg aag aag att agt gca atc att gan gaa gag gaa gaa gat gga agc  
912

Trp Lys Lys Ile Ser Ala Ile Ile Xaa Glu Glu Glu Glu Asp Gly Ser  
290 295 300

tga  
915

<210> 7  
<211> 304  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (1)...(304)  
<223> Xaa = Any Amino Acid

<400> 7

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Lys	Ala	Asp	Cys	Pro	Thr	Met	Glu	Ala	Gln	Thr	Thr	Leu	Thr	Thr	Asn
			20					25					30		
Asp	Ile	Val	Ile	Ser	Lys	Leu	Thr	Gln	Ile	Leu	Ser	Tyr	Leu	Arg	Gln
		35					40					45			
Gly	Thr	Arg	Asn	Lys	Lys	Leu	Lys	Lys	Lys	Asp	Lys	Gly	Lys	Pro	Glu
	50					55				60					
Glu	Lys	Lys	Pro	Pro	Glu	Ala	Asp	Met	Asn	Ile	Phe	Glu	Asp	Ile	Gly
65					70					75					80
Asp	Tyr	Val	Pro	Ser	Thr	Thr	Lys	Thr	Pro	Arg	Asp	Lys	Glu	Arg	Glu
				85					90					95	
Arg	Tyr	Arg	Glu	Arg	Glu	Arg	Asp	Arg	Glu	Arg	Asp	Arg	Asp	Arg	Asp
			100					105					110		
Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp
			115					120					125		
Arg	Glu	Arg	Glu	Glu	Glu	Lys	Lys	Arg	His	Ser	Tyr	Phe	Glu	Lys	Pro
			130				135				140				
Lys	Val	Asp	Asp	Glu	Pro	Met	Asp	Val	Asp	Lys	Gly	Pro	Gly	Ser	Thr
145					150					155					160
Lys	Glu	Leu	Ile	Lys	Ser	Ile	Asn	Glu	Lys	Phe	Ala	Gly	Ser	Ala	Gly
				165					170					175	

Trp	Glu	Gly	Thr	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Asp	Lys	Lys	Gln	Leu
			180					185					190		
Gly	Asp	Phe	Phe	Gly	Met	Ser	Asn	Ser	Tyr	Ala	Glu	Cys	Tyr	Pro	Ala
		195					200					205			
Thr	Met	Asp	Asp	Met	Ala	Val	Asp	Ser	Asp	Glu	Glu	Val	Asp	Tyr	Ser
	210					215					220				
Lys	Met	Asp	Gln	Gly	Asn	Lys	Lys	Gly	Pro	Leu	Gly	Arg	Trp	Asp	Phe
225					230					235					240
Asp	Thr	Gln	Glu	Glu	Tyr	Ser	Glu	Tyr	Met	Asn	Asn	Lys	Glu	Ala	Leu
			245					250						255	
Pro	Lys	Ala	Ala	Phe	Gln	Tyr	Gly	Ile	Lys	Met	Ser	Glu	Gly	Arg	Lys
			260					265					270		
Thr	Arg	Arg	Phe	Lys	Glu	Thr	Asn	Asp	Lys	Ala	Glu	Leu	Asp	Arg	Gln
		275					280					285			
Trp	Lys	Lys	Ile	Ser	Ala	Ile	Ile	Xaa	Glu	Glu	Glu	Glu	Asp	Gly	Ser
	290					295					300				

<210> 8  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

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 1 5 10 15

□